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## PM9444R UI·M·EH IMAGE:5 BM94445 RM944445 FST 52 1 R2F bp mPNA linear EST 14-MAP-2002 HCp-bur-i-02 C UI.r1 NIH\_EMAF\_EHCF Mus mustulus cDNA clone 5695945 57, mRNA sequence. 52

ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL COMMENT

KEYWOPDS SOURCE OPGANISM

house

mouse

GI-1942R037

ACCESSION VERSION

RESULT 1 BM944452 LOCUS DEFINITION

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 826)
NIH MGC http://mgc nci nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus Collection

Gene

found this (AVM)

This continue this continue the continu Contact Email: Tissue cDNA I cDNA I cNA Se act: Robert Strausberg, Ph.D.

1: cgapbs-r@mail.nih.gov

1: cgapbs-r@mail.nih.gov

2: Produrement. Dr. James Tin, Univeristy of Towa

3: Library preparation: Dr. M. Bento Scares, Univeristy of Towa

4: Library Arrayed by: Dr. M. Bento Scares, Univeristy of Iowa

5: Sequencing by: Dr. M. Bento Scares, Univeristy of Towa

6: Sequencing by: Dr. M. Bento Scares, Univeristy of Towa

7: Sequencing by: Dr. M. Bento Scares, Univeristy of Towa

8: Sequencing by: Dr. M. Bento Scares, Univeristy of Towa

9: Sequencing by: Dr. M. Bento Scares, Univeristy of Towa

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1: A through the T.M.A.G E. Conscrtium/TIML at:

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/strain="C57BL/6"
/db_kr=f="taxon-ioogo"
/clone-"TMAGE:[695945"
/clone_lib="NIH_BMAP_EHOp"
/tissue_type="whole_brain"
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Isolation of full-length cDNA clones from a mouse brain cDN library made by oligo-capping method unpublished (1999)
Contact Eatsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1 chome, shinjuku ku, Tokyo 162-6640, Japan Email: khashiwnih.go.jp
TPL http://www.hih.go.jp
TPL http://www.hih.go.jp
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malia, Eutheria, Rodontia, Sciurognathi; Muridao; Murinae; Mus
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al Similarity 96.3%;
182; Conservative
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Io
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Io
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
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NIH MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian
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This clone was contributed by the Brain Molecular Anatomy Project
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Contact: Rol
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/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/note="Organ. brain; Vector: pX:Asc; Site_1. EcoR I,
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Jen.mu Research, 6.731 806,
1906 Denarged mpNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is CAGCCACGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Mervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5686584"
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National Institute of Infectious Diseases
23 1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640,
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Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                              /strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCb-3469"
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/sex="female"
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S Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramote, E., Hori, F., Ishii, Y., Ito, Y., Fawai, J., Front, H., Fooda, M., F., S., Matalyana, T., Miyutaki, A., Menuta, F., Choo, M., Fooda Okazayi, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shinagawa, Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

L. Unpublished (2001)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                              Computer-based methods for the mouse full-length cDNA entyplopedia, real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) . Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Senome Sequences. Manm. Senome. 12, 613-677 (2001) . Please visit out web site (http://genome.gsc.riken.go.jp) for
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GSS; genome survey sequence.
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AL305377.1 31.8137183
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii,
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3 (bases 1 to 752)

Genoscope.

Direct Submission
Submitted (12 APR 2000)

This sequence is a single r
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Location/Qualifiers
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2 (bases 1 to 752)

2 bases 1 to 752)

Roest-Crollius, H., Jaillon, O., Dasilva
Bouneau, L., Billault, A., Quetier, F., Sa
Weissenbach, J.

Charaterization and repeat analysis of
freshwater pufferfish Tetraodon nigrov
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Saurin,W. and Weissenbach,J.
Human gene number estimate provided
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Charaterization and repeat analysis of the r
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Tetraedentidae; Tetraeden.

(bases 1 to 802)

Reest-Crellius, H., Jaillon, O., Dasilva, C., Rouneau, L., Fisher, C., Rernet, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
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Location/Qualifiers
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/db_xref="taxon:99883"
/clone="007D16"
/clone_lib="H"
/clone_lib="H"
/note="Genoscope sequence ID : CORHOOTDBORXD1~end
/note="Genoscope sequence ID : CORHOOTDBORXD1~end
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Unpublished (1998)
Contact. Stephen L. Johnson
Washington University School of Medicine
4444 Forest Fark Parkway, Fox 8501, St. 1
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library freparation. Ming Wu. cDNA Library Arrayed by. Steve Johnson DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Research Genetics web address: http://www.research.genetics.org/
Possible reversed clone. similarity on wrong strand
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Clark,M., Johnson,S.L., Lebrach,H., Leo,R., Li,F., Marra,M., Eddy,J., Hiller,L., Eusaka,T., Martin,C., Beck,T., Wylie,T., Tolerwoo,,E., Steptue,M., Theising,E., Allen,M., Edwers,T., Ferson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilsun,R.
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High quality sequence stop: 431
Location/Qualifiers
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Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
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Actisopterygii, Neogterygii, Teleostei, Octariophysi,
; Cyprinidae; Danio.
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(clone_lib="Zebrafish Research Genetics C32 fin"

(tissue_type="Fin"

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GSS; genome survey sequence.
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Tetra-don nigroviridis
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Acanthomorpha; Acanthopterygil, Tele stelly Erelested, Menteleosted;
Tetracdontidae; Tetracdon
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fi
Rouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
Weissenbach, J.
Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetrandon nigroviridis
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Lecation/Qualifiers
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/db_xref="taxon:99883"
/clone="184E16"
/clone_lib="G"
/note "Jenoscope sequence ID . C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WashU Zebrafish EST Project 1998
Unpublished (1998)
Other ESTs: fm97a09.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Lou
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson wustl edu
                                                                                                                                                      158; Conservative
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Possible reversed clone: similarity on wrong strand High quality sequence stop: 467.
Location/Qualifiers
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Clark,M , Johnson,S.L., Lehrach,H., Lee,P., Li,F , Marra,M , Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptce,M., Theising,B., Allen,M., Powers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,P., Waterston,Pand Wilson,R.
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fm97309 yl Zebrafish Research Genetics
clone 4468528 5' similar to TR.Q9Y2DF
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Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
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Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_hos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="4468528"
/clone_lib-"Zebrafish Research Genetics C32 fin"
/tissue_type="Fin"
/lab_host="GeneHogs (HS996, a phage-resistant isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
/db_xref="taxon:7955"
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Poest-Crollius; H., Jaillon; O., Dasilva; C., Rouneau, L., Fisher; C., Bernot, A., Fizames; C., Wincker, F., Brottier, F., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by gonome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                          genome.
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Submitt
This se
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Tetraodon nigroviridis genome survey sequence PMC-Ori and of clone
231000 of library G from Tetraodon nigroviridis, genomic survey
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st-Crollius,H , Jaillon,O , Dasilva,C , Fizames,C , r
meau,I , Billault,A , Quetier,F , Saurin,W , Bernot,A
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/clone_lib="G"
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247 c 247 g 260 t
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|db_xref="taxon:99883"
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Unpublished (1997)
Contact. Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LIMI, contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 356.
Location/Qualifiers
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Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi Chases 1 to 436)

1 (bases 1 to 436)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Hillier,L., Rucubu,T., Lasy,M., Le,N., Lennon,S., Maria,M., Marian,L., Kucubu,T., Lasy,M., Ethpioe,M., Tan,F., Theising,R., J., Moore,B., Schellenberg,K., Stepioe,M., Tan,F., Theising,R., White,Y., Wylie,T., Waterston,P. and Wilson,R
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ue/lid4.si Stratagone schizo krain E11 Homo sapiens cDNA clone
IMACE.969607 37 similar to TR:3205716 G205716 NEURBXIN II ALPHA A
PRECURSOR. ;, mRNA sequence.
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                             /tissue_type="schizophrenic brain 3:11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
/note:"Vector. Rluestript SK, Site_1 Ener, Library
/note:"Vector. Rluestript SK, Site_1 Ener, Library
constructed from S-11 frontal lobe, male, 34 years old,
5:% narmasian, Sek Aleutian Schizophrenic scinide
Random primed into EcoRI site of ZAF II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Constition Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Thpublished) Stanley Neuropathology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
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/db_xref="taxon:9606"
/ci_ne="IMAGE.j&j&j&;"
/clone_lib="Stratagene schizo brain Sll"
/sex="male"
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Fahronkrug,S C., Freking,B.A., Pohrer,G.A., Smith,T. Stone,B.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.W.
Design and use of two pooled tissue normalized oDNA
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Single pass sequencing. Bases called
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and -minmatch 12 options.
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/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
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/tissue_type="pooled"
/tissue_type="pooled"
/lab_host="DH19B"
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El (bases 1 to 655)

Nonneman,D.J. and Waldbieser,G.C.
(Ictalurus punctatus)

Unpublished (2002)
Contact: Waldbieser GC
Catfish Genetics Research Unit
USDA-Agricultural Research Service
141 Experiment Station Road, Stoneville, MS 38776, USA
Tel: 662 686 3567
Email: gwaldbieser@ors usda gov
Single pass sequencing Bases ralled with Phred vo.000925 c
quality bases and vector trimmed with Lucy v1.16.
Plate: Brl 15 row: F column: 5
Seq primer: M12 Reverse.
Location/Qualifiers
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/strain="USDA103"
/db_xref="taxon:7998"
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GSS; genome survey sequence.
Tetracdon nigroviridis.
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Submitted (12-APP-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon
Location/Qualifiers
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Human gene number estimate provided by genome workeraodon nigroviridis DNA sequence
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Weissenbach, J.

Charaterization and repeat analysis of the compact
freshwater pufferfish Tetraodon nigroviridis
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Actinopterygii; Neopterygii; Teleostei, Euteleostei; Neoteleostei;
Acanthomorphu, Acanthorterygii, Person izha, Tetrandontiformes;
Tetraodontidae; Tetraodon.
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rollins,H , daillon,O
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/db_xref="taxon:99883"
/clone="140106"
/clone_lib="G"
/note="Genoscope seguence ID - ToA/
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